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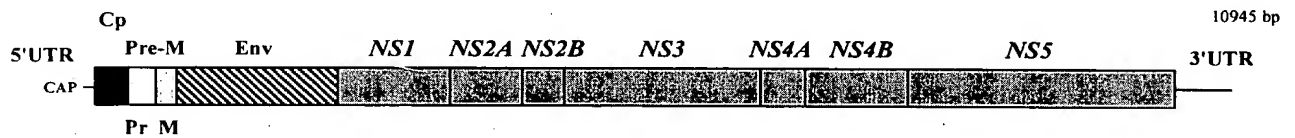
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Genomic organization of WNV-HNY1999



Cloning Strategy for WNV-HNY1999 Capsid Gene: pWNVh-DJY, pWNVy-DJY

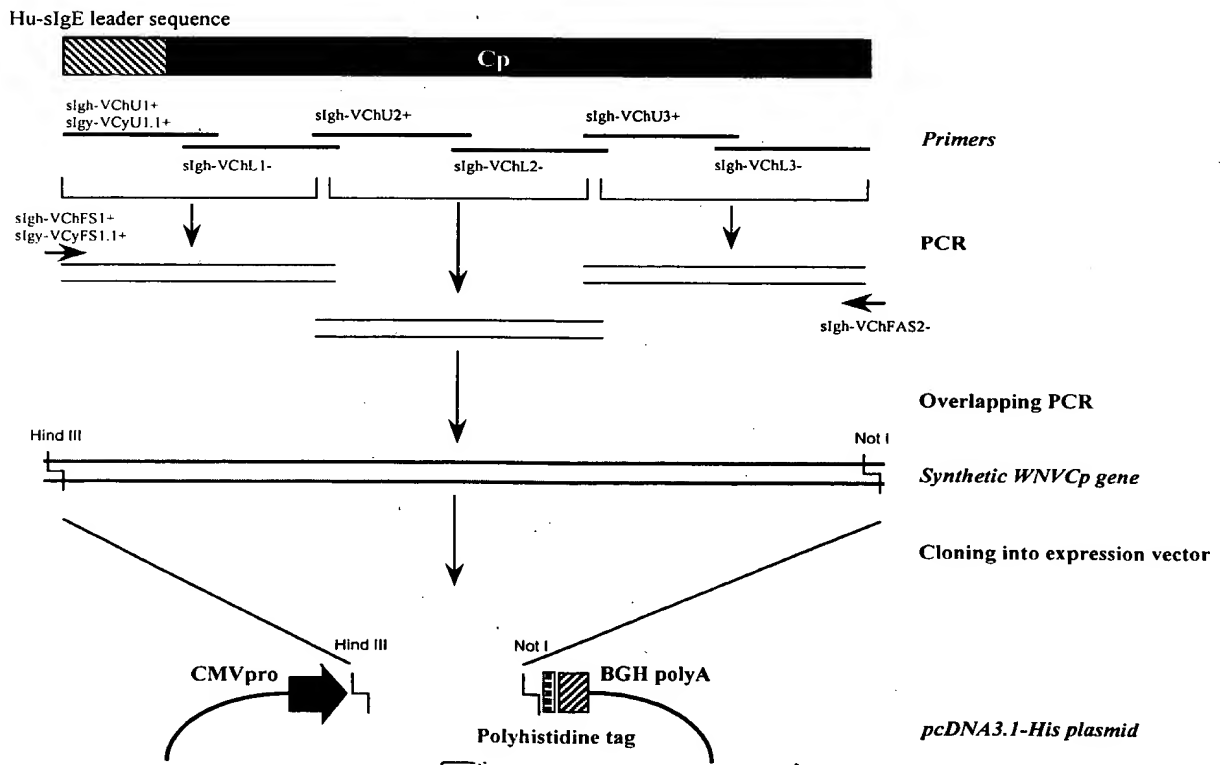


FIG 1

pWNVh-DJY Cut site Map
Tuesday, September 5, 2000 2:09 PM

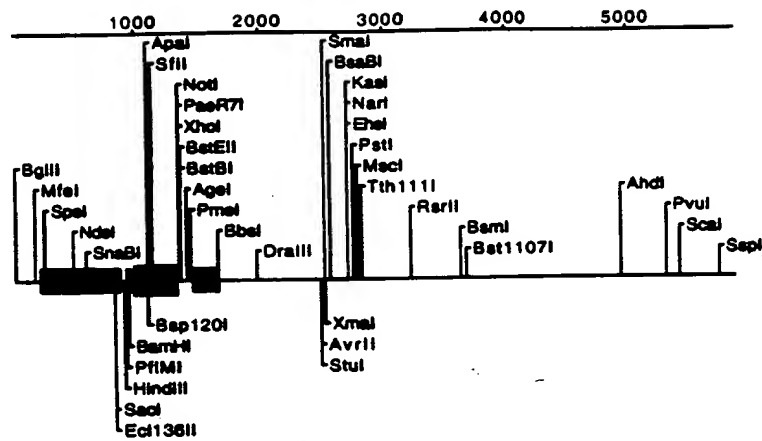


FIG. 2

pWNVh-DJY Cut Site Map
Tuesday, September 5, 2000 2:09 PM

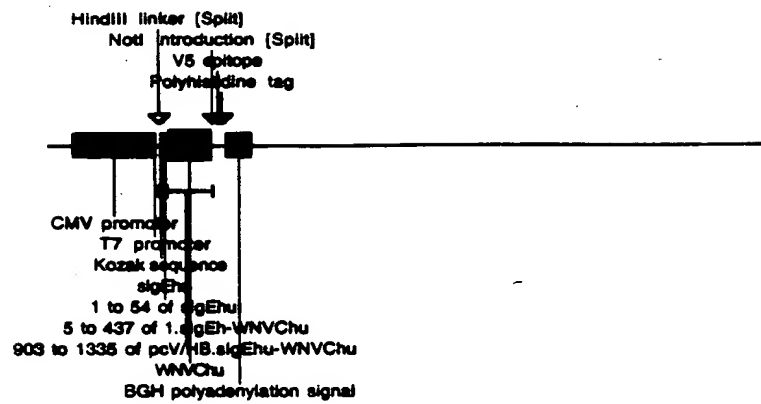


FIG. 3

Sequence Range: 1 to 5864

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CTGCCTAGCCCTCTAGAGGGCTAGGGGATACCAGCTGAGAGTCATGTTAGACGAGACTACGGCGTATCAATTCCGTCATAGACGAGGGACGAACACACAA

>MfeI
110 120 130 140 150 160 170 180 190 200
GGAGGTCGCTGAGTAGTGCAGGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGACAATTGCGATGAAGAATCTGCTTAGGGTTAGGCGTTTTCGG
CTCCAGCGACTCATCACGCGCTCGTTTAAATTCGATGTTGTTCCGTTCCGAACGGCTGTTAAGTACTTCTTAGACGAATCCAATCCGCAAAACGC

>SpeI
210 220 230 240 250 260 270 280 290 300
CTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATTATTGACTAGTTAATAAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATA
GACGAAGCGCTACATGCCCCGTCTATATGCGCACTGTAACATAAATGATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATAT

310 320 330 340 350 360 370 380 390 400
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ACCTCAAGGCGCAATGTATTGAATGCCATTACCGGGCGGACCGACTGGCGGGTGTCTGGGGCGGGTAACGTCAGTTATTACTGCATACAAGGTATCA

>NdeI
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>SnaBI
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GGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCACTGACTGGAATACCCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGT

610 620 630 640 650 660 670 680 690 700
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AGCGATAAATGGTACCCTACGCCAAACCGTCATGTAGTTACCCGCACTTACGCCAACTGAGTGGCCCTAAAGGTTACAGAGGTGGGGTAACGTCAGTT

710 720 730 740 750 760 770 780 790 800
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ACCCCTCAACAAACCGTGGTTTGTAGTTGCCCTGAAAGGTTTACACGATTGTTGAGGCGGGTAACGTCGCTTACCCGCATCCGCACATGCCACCCTC

>SacI
>Ecl136II
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>Kozak_sequence
>HindIII_linker (Split)
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ATTGGAACCGCGGTGTTACCTGACCTGGACCTAGGACAAGGACCAACCGCGCGCGTGGCGCACGTGTGAGATTCTTTGGTCTCCGGGCGGTCTCTCG
M D W T W I L F L V A A A T R V H S>
SIGEHU
S K K P G G P G K S>
WNVCHU
910 920 930 903 TO 1335 OF PCV/HB.SIGEHU-WNVCHU_0 980 990 1000>
10 20 30 5 TO 437 OF 1.SIGEH-WNVCHU_70 80 90 100>
10 10 1 TO 54 OF SIGEHU_40 50>

>PflMI
>BamHI
>T7_promoter
860 870 880 890 900
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CAGATATATTCTGCTCTGAGAGACCGATTGATCTCTTGGGTGACGAATGACCGAATAGCTTTAATTATGCTGAGTGATATCCCTCTGGGTTTCGACCGATCA

>HindIII
>Kozak_sequence
>HindIII_linker (Split)
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ATTGGAACCGCGGTGTTACCTGACCTGGACCTAGGACAAGGACCAACCGCGCGCGTGGCGCACGTGTGAGATTCTTTGGTCTCCGGGCGGTCTCTCG
M D W T W I L F L V A A A T R V H S>
SIGEHU
S K K P G G P G K S>
WNVCHU
910 920 930 903 TO 1335 OF PCV/HB.SIGEHU-WNVCHU_0 980 990 1000>
10 20 30 5 TO 437 OF 1.SIGEH-WNVCHU_70 80 90 100>
10 10 1 TO 54 OF SIGEHU_40 50>

>ApaI
>Bsp120I
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
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GGCGGGCACTTGTACGACTTCGCGCGCTACCGGGCGCACGACTCGGACTAACCGGACTTCGCGCGGTACGACTCGGACTAGCTGCGCTTCCGGGCTATG
R A V N M L K R G M P R V L S L I G L K R A M L S L I D G K G P I>
WNVCHU
1010 1020 1030 903 TO 1335 OF PCV/HB.SIGEHU-WNVCHU_70 1080 1090 1100>
110 120 130 5 TO 437 OF 1.SIGEH-WNVCHU_170 180 190 200>

>SfiI
1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
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CGAAGCACGACCGGGACGACCGGAAGAGGCGAAGTGGCGGTAAACGGGGTGGCGCGGCACGACTGGCGACCGCGCGCACTTGTCTGCTGGCGGTA
R F V L A L L A P F R P T A I A P T R A V L D R W R G V N K Q T A M>
```

Fig 4

WNVCHU
1110 1120 1130 903 TO 1335 OF PCV/HB. SIGEHU-WNVCHU_70 1180 1190 1200
210 220 230 5 TO 437 OF 1.SIGEH-WNVCHU_270 280 290 300
1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
GAAGCACCTGCTGAGCTTCAAGAAGGAGCTGGGACCCCTGACCAGCGCCATCAACCGCCGAGCAGCAAGCAGAAGAGCGCGCGGCAAGACCGGCATT
CTTCGTGGACGACTCGAAGTCTTCTCTCGACCCGCTGGGACTGGTGGCGGTAGTTGGCGGGCTCGTCTGCTTCTTCGCGCCCGCTTCTGGCCGTAA
K H L L S F K K E L G T L T S A I N R R S S K Q K K R G G K T G I
WNVCHU
1210 1220 1230 903 TO 1335 OF PCV/HB. SIGEHU-WNVCHU_70 1280 1290 1300
310 320 330 5 TO 437 OF 1.SIGEH-WNVCHU_370 380 390 400
>BstEII
>PaeR7I
>NotI
>NotI_introduction_[Split]
>XhoI
>BstBI
>V5_epitope
1310 1320 1330 1340 1350 1360 1370 1380 1390 1400
GCCGTGATGATTGGCCTGATCGCCAGCGTGGGCGCGCGCGCTCGAGGTCAACCCATTCGAAGGTAAGCCTATCCCTAACCCCTCTCTCGGTCTCGATTCTA
CGGCACTACTAACCGGACTAGCGGTGCGCACCCGCGCGCGGAGCTCCAGTGGGTAAAGCTTCCATTCGGATAGGATTGGGAGAGGAGCCAGAGCTAAGAT
A V M I G L I A S V G A
WNVCHU
903 TO 1335 OF PCV/HB. SIGEHU
5 TO 437 OF 1.SIGEH-WNVCHU
>AgeI
>PaeI
>Polyhistidine_tag
>BGH_polyadenylation_signal
1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
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GGCGATGGCCAGTAGTAGTGGTAGTAACTCAAATTTGGGCGACTAGTCCGAGCTGACACGGAAGATCAACGGTCCGTAGACAACAAACGGGAGGGG
1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
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GCACGGAAGAACTGGGACCTTCCACGGTGAGGTGACAGGAAAGGATTATTTACTCCTTTAACGTAGCGTAACAGACTCATCCACAGTAAGATAAGAC
>BbsI
1610 1620 1630 1640 1650 1660 1670 1680 1690 1700
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1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
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GGTCGACCCCGAGATCCCCATAGGGGTGCGGGGACATCGCCCGTAATTTCGCGCGCCACACCAATGCGCGTCCGACTGGCGATGTGAACGGTC
1810 1820 1830 1840 1850 1860 1870 1880 1890 1900
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CGGGATCGCGGGCAGGAAAGCGAAAGAGGAAAGAGCGGTGCAAGCGCGCGGAAAGGGGAGTTTCGAGATTAGCCCGCTAGGGAATCCCAAG
>DraIII
1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
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GCTAAATCACGAAATGCGGTGGAGCTGGGGTTTTTGAATAATCCCACTACCAAGTGATCACCCTGAGCGGACTATCTGCCAAAAAGCGGAAACT
2010 2020 2030 2040 2050 2060 2070 2080 2090 2100
CGTTGGAGTCCAGCTTCTTTAATAGTGGACTCTGTGTTCAAACTGGAACAACACTCAACCTATCTCGGTCTATTCTTTTATTATAAGGGATTTTGGG
GCAACCTCAGGTGCAAGAAATATCACTTGAGAACAAAGGTTTGACCTTGTGTGAGTTGGGATAGAGCCAGATAAGAAAACTAAATATTCCCTAAACCC
2110 2120 2130 2140 2150 2160 2170 2180 2190 2200
GATTTCCGGCTATTGGTTAAAAATGAGCTGATTTAAACAAAAATTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAGTCCCCAG
CTAAAGCCGGATAACCAATTTTTTACTCGACTAAATTTGTTTTAAATTCGCTTAATTAAGACACCTTACACACAGTCAATCCACACCTTTTCAGGGGTC
2210 2220 2230 2240 2250 2260 2270 2280 2290 2300
GCTCCCCAGGCGAGGAGATGCAAAAGCATGCAATCTCAATTAGTCAGCAACAGGTGTGGAAGTCCCGAGGCTCCCGAGGAGGAGGATGCAAA
CGAGGGGTCCTGCGTCTCATACGTTTCGTACGTAGAGTTAATCAGTCGTGTGTCACACCTTTCAGGGGTCGAGGGGTCGTCTTCATACGTTT
2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
GCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCGCGCCATCCCGCCCTAACTCCGCGGAGTTCGCGCCATTTCTCCGCCCATGGGCTG
CGTACGTAGAGTTAATCAGTCGTGTGTTATCAGGCGGGGATTGAGGCGGGTATGAGGCGGGTCAAGGCGGGTAAGAGCGGGGATCCGAC
>AvrII
>StuI
2410 2420 2430 2440 2450 2460 2470 2480 2490 2500
ACTAATTTTTTTTATTTATGACAGGCGGAGGCGGCTCTGCTCTGAGCTATTCCAGAAAGTAGTGAGGAGGCTTTTTTGGAGGCTTAGGCTTTTGCAAA
TGATTAATAAATAAATACGTCTCCGCTCCGCGGAGACGAGACTCGATAAGGTCTTCATCACTCTCTCGAAAAACCTCCGGATCCGAAAAAGCTTT
>SmaI
>XmaI
>BsaBI
2510 2520 2530 2540 2550 2560 2570 2580 2590 2600
AAGCTCCCGGAGCTGTATATCCATTTCGGATCTGATCAAGAGACAGGATGAGGATCGTTTCGATGATTGAACAAGATGGATTGCAAGCAGGTTCTC
TTCAGGGGCTCGAACATATAGGTAAGGCTAGACTAGTTCTCTGCTCTACTCTAGCAAGCGTACTAATCTGTTCTACCTAACGTCGCTCAAGAG

4510 4520 4530 4540 4550 4560 4570 4580 4590 4600
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CACGATGCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCCTGTCTATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTC
4610 4620 4630 4640 4650 4660 4670 4680 4690 4700
AGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTGTTTGTGTTTGGCAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAA
TCAACCATCGAGAACTAGGCGCTTTGTTTGGTGGCGACCATCGCCACCAAAAAACAAACGTTCTGCTCTAATGCGCGTCTTTTTCCTAGAGTTCTT
4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
GATCCTTTGATCTTTTCTACGGGGTCTGACCGCTCAGTGGAAACGAAACTCACGTTAAGGGATTGTTGTCATGAGATTATCAAAAAAGGATCTTCACCTAGA
CTAGGAAACTAGAAAAAGATGCCCGAGACTGCGAGTCACTTGTCTTTGAGTGCAATTCCTAAAACAGTACTCTAATAGTTTTTCTAGAAAGTGGATCT
4810 4820 4830 4840 4850 4860 4870 4880 4890 4900
TCCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAAGGCACCTATCTC
AGGAAAAATTAAATTTTACTTCAAAATTAGTTAGATTTCATATATACTCATTTGAACAGACTGTCTCAATGGTTACGAATTAGTCACTCCGTGGATAGAG
4910 4920 4930 4940 4950 4960 4970 4980 4990 5000
AGCGATCTGCTATTTTCGTTTCATCTAGTTGCTGCTGACTCCCGCTCGTGTAGATACTAGCATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATG
TCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGAGCAGACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGTCAACGCTTAC
5010 5020 5030 5040 5050 5060 5070 5080 5090 5100
ATACCGCGAGAGCCACGCTCACCGGCTCCAGATTTCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAAGTGGTCTGCAACTTTATCCGCT
TATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCTGTTATTTGGTGGTGGCGCTTCCCGGCTCGCGTCTTCCACGAGACGTTGAAATAGGCGGA
5110 5120 5130 5140 5150 5160 5170 5180 5190 5200
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GGTAGGTCAAGATAATTAACAAACGCGCTTCGATCTCATTCATCAAGCGGTCAATATCAAAACGCGTTGCAACACGGAACGATGTCGTAGCACCACAG
5210 5220 5230 5240 5250 5260 5270 5280 5290 5300
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TGGCAGCAGCAAAACCATACCGAAGTAAGTCGAGGCCAAGGGTGTCTAGTTCCGCTCAATGTACTAGGGGGTACAAACAGCTTTTTCGCAATCGAGGAAG
5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
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CCAGGAGGCTAGCAACAGTCTTCACTCAACCGCGCTCACAAATAGTGAGTACCAATACCGTCGTGACGTATTAGAGAAATGACAGTACGGTAGGCATTCTA
5410 5420 5430 5440 5450 5460 5470 5480 5490 5500
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CGAAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATACCGCGCTGGCTCAACGAGAACGGGCGCAGTTATGCCCTATTATGGCG
5510 5520 5530 5540 5550 5560 5570 5580 5590 5600
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CGGTGTATCGTCTTGAAATTTTACGAGTAGTAACCTTTTGAAGAAAGCCCGCTTTTGAAGTCTCTAGAAATGGCGACAACCTTAGGTCAAGCTACATT
5610 5620 5630 5640 5650 5660 5670 5680 5690 5700
CCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAA
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5710 5720 5730 5740 5750 5760 5770 5780 5790 5800
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CCCGCTGTGCTTTACAACTTATGAGTATGAGAAAGGAAAAAGTTATAATAACTTCGTAATAGTCCCAATAACAGAGTACTCGCTATGTATAAACTTAC
5810 5820 5830 5840 5850 5860
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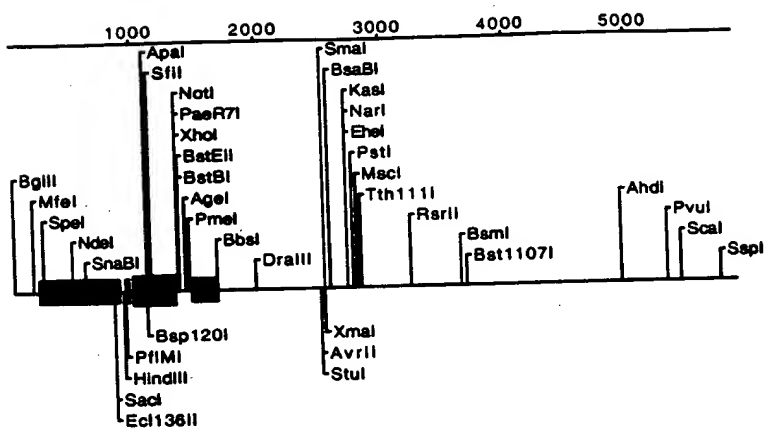


Fig. 5

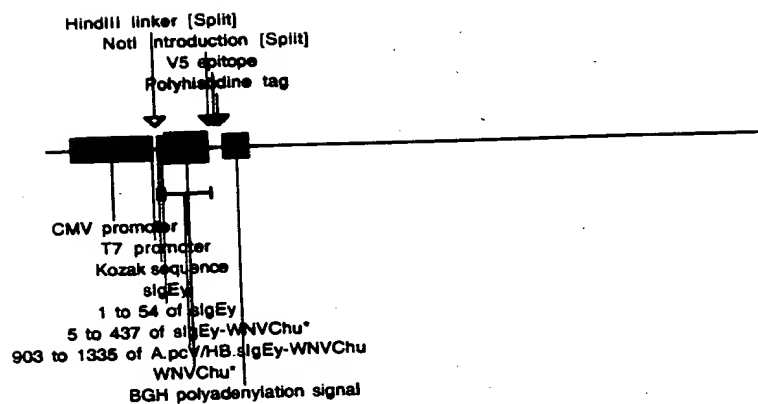


FIG. 6

Sequence Range: 1 to 5864

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CTGCTAGCCCTCTAGAGGGCTAGGGGATACAGCTGAGAGTCATGTTAGACGAGACTACGGCTATCAATTCGGTCATAGACGAGGGACGAACACACAA

>MfeI
110 120 130 140 150 160 170 180 190 200
GGAGGTCTGCTGAGTAGTCCGCGAGCAAAATTTAAGCTACAACAAGCGAAGCCTTGACCGACAATTCGATGAAGAACTCTGCTTAGGGTTAGGCGTTTTCGG
CCTCCAGCGACTCATCACGCGCTCGTTTAAATTCGATGTTGTTCCGTTCCGAACGGCTGTTAAGTACTTCTTAGACGAATCCCAATCCGCAAAACGC

>SpeI
210 220 230 240 250 260 270 280 290 300
CTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTTACGCCATATA
GACGAAGCGCTACATGCCCGTCTATATGCGCAACTGTAATAAAGTATCAATTAATGATTAATGCCCCAGTAATCAAGTATCGGGTATAT

>CHV_promoter
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ACCTCAAGCGCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGCGGGTTCGTTGGGGCGGGTAAGTGCAGTTATTACTGCATACAAAGGTATCA

>NdeI
410 420 430 440 450 460 470 480 490 500
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TTCCGGTTATCCCTGAAAGGTAAGTGCAGTTACCCACCTGATAAATGCCATTTGACGGGTGAACCGTCATGTAGTTACATAGTATACGGTTTCATGCGGG

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GGATAAATGCAGTTACTGCCATTTACCGGGCGGACCGTAAATACGGGTCTATGTAAGTACCCCTGAAAGGATGAACCGTCAATGATGATAATCAATCAAT

610 620 630 640 650 660 670 680 690 700
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AGCGATAATGGTACCACCTACGCCAAAACCGTCATGTAGTTACCCGACCTATCGCCAAACTGAGTGGCCCTAAAGGTTACAGAGTGGGGTAACTGCAGTT

710 720 730 740 750 760 770 780 790 800
TGGGAGTTTGTTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCTGAACAACTCCGCCCATTTGACGCAAAATGGGCGGTAGGCGGTGATCGGTGGGAG
ACCCCTAAACAAAACCGTGGTTTGTAGTTCCCTGAAAGGTTTACAGCATTTGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCTC

>SacI
810 820 830 840 850 860 870 880 890 900
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CAGATATATTGCTCTGAGAGACCGATTGATCTCTTGGGTGACGAATGACCGAATAGCTTTAATTATGCTGAGTGATATCCCTCTGGGTTCCGACCGATCA

>HindIII
910 920 930 940 950 960 970 980 990 1000
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ATTCGAACGGCGGTGGTACCTAACCTGAACCTAGAATAAAAAATCAACGACGACGATGATCTCAAGTAAGAAGATTTTGTGTCACCGGGGCGGTCTCTCG
M D W T W I L F L V A A A T R V H S>
SIGEY>
S K K P G G P G K S>
910 920 930 903 TO 1335 OF A. PCV/HB. SIGEY-WNVCHU_0 980 990 1000>
10 20 30 4.5 TO 437 OF SIGEY-WNVCHU_0 70 80 90 100>
10 10 1 TO 54 OF SIGEY_40 50>

>Pf1MI
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>HindIII_linker (Split)
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
CGCGCCGTGAACATGCTGAAGCGCGGCATGCCCGCGCTGCTGAGCCTGATTTGGCTTGAAGCGCGCCATGCTGAGCCTGATCGACGGCAAGGGCCCCATAC
GCGCGCACTTGTACGACTTCGCGCCCTACGGGGCGGCACTCGGACTAACCGGACTTCGCGCGGTACGACTCGGACTAGCTGCCGTTCGCGGGTATG
R A V N M L K R G M P R V L S L I G L K R A M L S L I D G K G P I>
WNVCHU>
1010 1020 1030 903 TO 1335 OF A. PCV/HB. SIGEY-WNVCHU_70 1080 1090 1100>
110 120 130 1.5 TO 437 OF SIGEY-WNVCHU_0 170 180 190 200>

>SfiI
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CGAAGCAGGACCGGGACCGGAAGGCGGAAGTGGCGGTAAACGGGGTGGCGCGCGGACGACCTGGCGACCGCGCGCACTTGTGCTGCGCGGTA
R F V L A L L A F F R P T A I A P T R A V L D R W R G V N K Q T A M>

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FIG 7

4510 4520 4530 4540 4550 4560 4570 4580 4590 4600
GTGCTACAGAGTCTTTGAAGTGGTGGCTTAACACGGCTACACTAGAAGGACAGATTATGGGTATCTGGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG
CACGATGTCTCAAGAATTCAACACCGGATTTGATGCCGATGTGATCTTCTGTCTATAAACCATAGACGGGAGACGACTTCGGTCAATGGAAGCCTTTTTC
4610 4620 4630 4640 4650 4660 4670 4680 4690 4700
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WNVCHU*
1110 1120 1130_903 TO 1335 OF A.PCV/HB.SIGBY-WNVCHU_70 1180 1190 1200
210 220 230 2_5 TO 437 OF SIGBY-WNVCHU* 270 280 290 300
1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
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K H L L S F K K E L G T L T S A I N R R S S K Q K K R G G K T G I
WNVCHU*
1210 1220 1230_903 TO 1335 OF A.PCV/HB.SIGBY-WNVCHU_70 1280 1290 1300
310 320 330 3_5 TO 437 OF SIGBY-WNVCHU* 370 380 390 400
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>PaeR7I
>NotI >XhoI >BstBI
>NotI_introduction_(Split) >V5_epitope
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A V M I G L I A S V G A
WNVCHU*
903 TO 1335 OF A.PCV/HB.SIGBY-WNVCHU*
5 TO 437 OF SIGBY-WNVCHU*
>AgeI >PmeI
>Polyhistidine_tag >BGH_polyadenylation_signal
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>StuI
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>MscI
>Tth111I
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**³⁵S-Labelled *in vitro* Translated Products of
pWNVCh-DJY and pWNVcy-DJY**

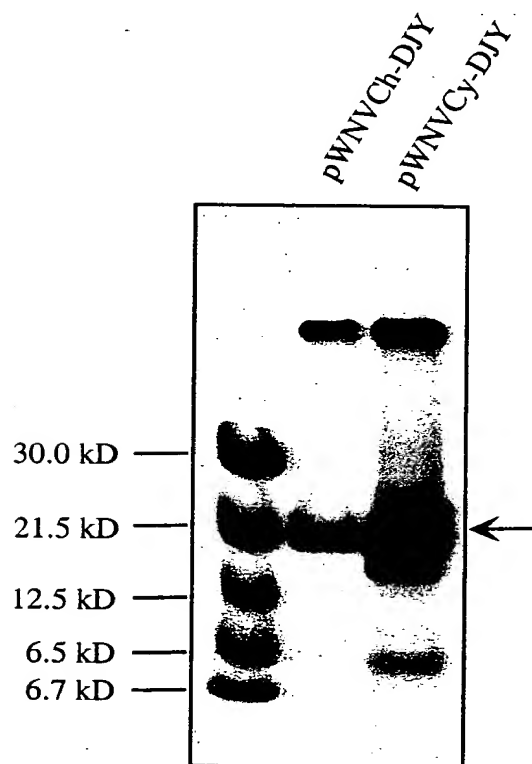


Fig 8

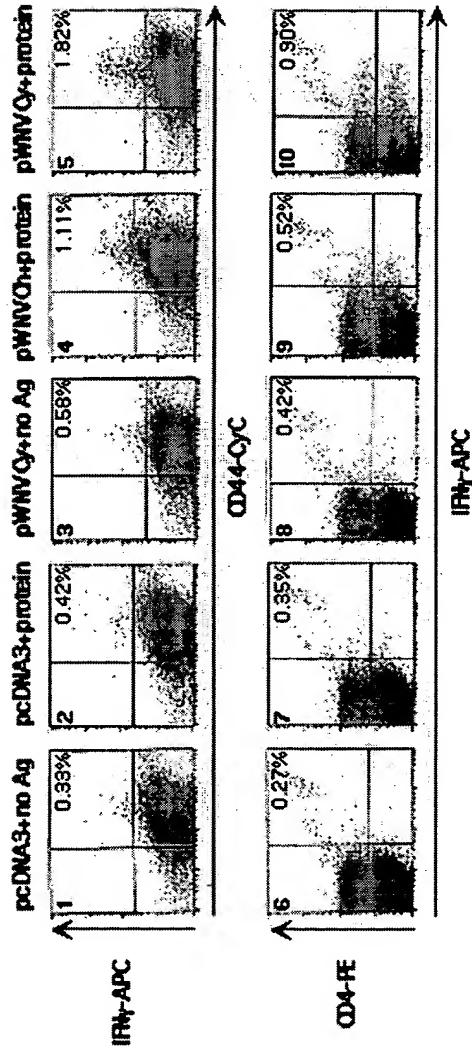
WNV Capsid (Cp) Peptides - Location and Sequences

WNV Cp Amino Acid Sequence	10	20	30	40	50	60	70	80	90	100	110	120
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Peptide Seq. Peptide Name	SKKPGGPGKSRVNNLKRGMPR WNV-C-P1											
	KRAMLSLIDGKGPIRFVLA WNV-C-P2											
	TLTSAINRRSSQKKRGGKTGTI WNV-C-P3											

Fig. 9

FIGURE 10

Fig. 10



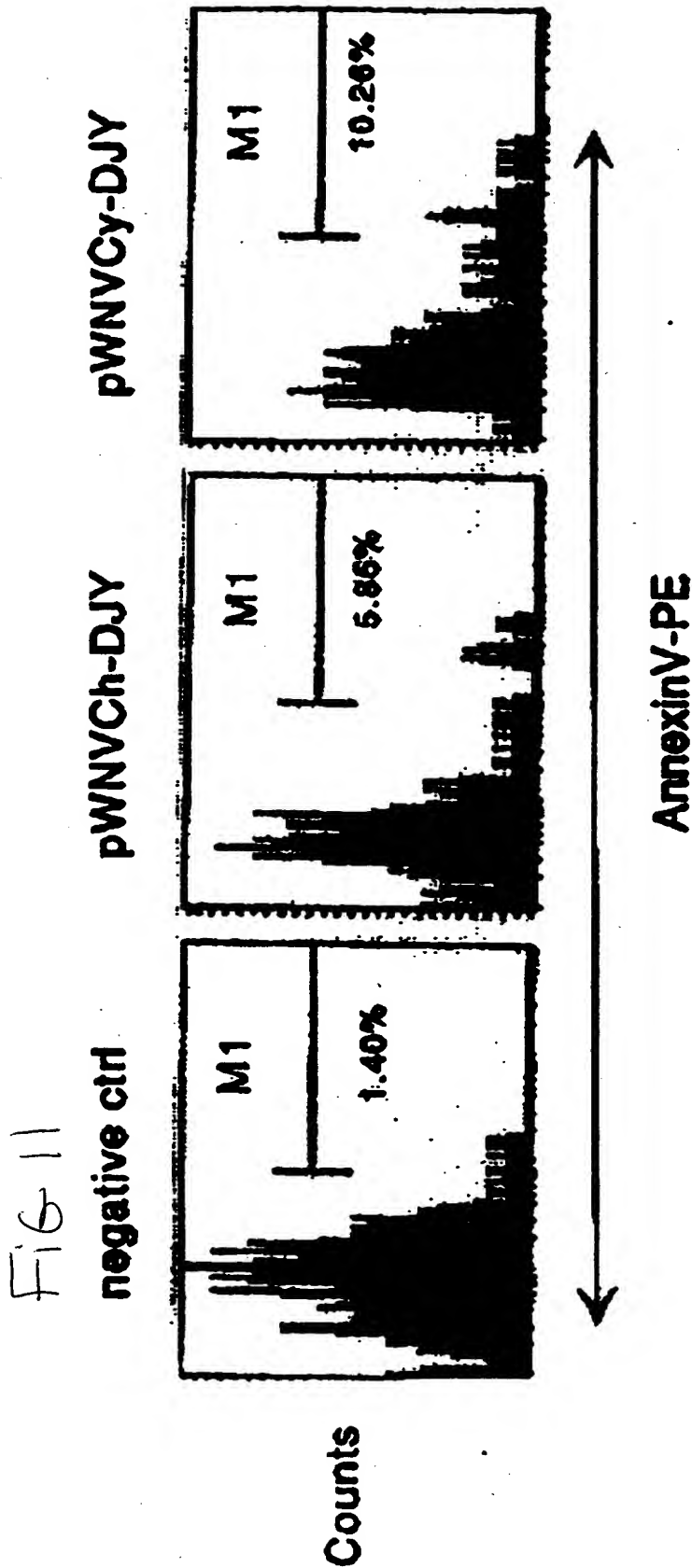


Fig. 12A

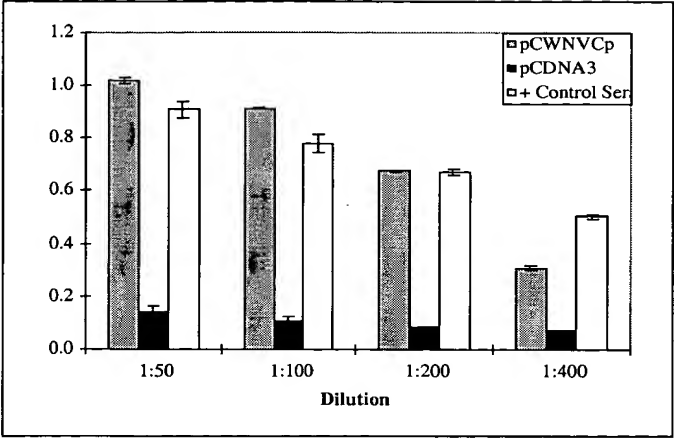


Fig. 12B

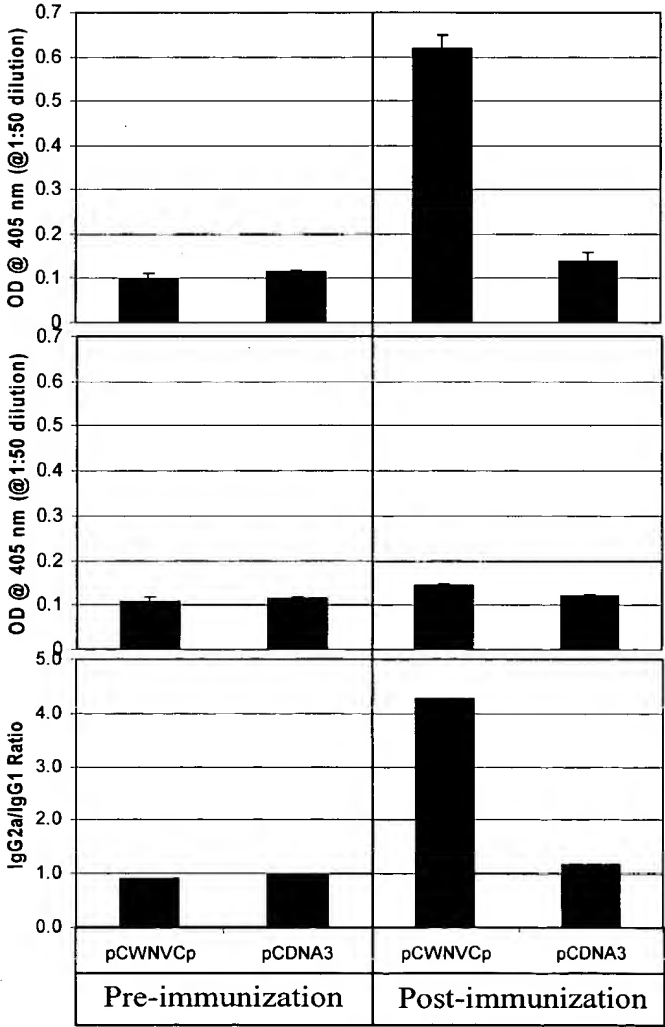
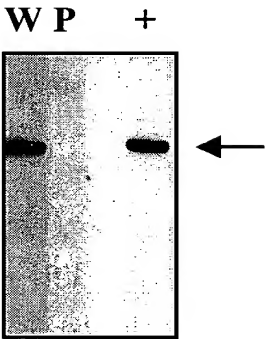


Fig. 12C



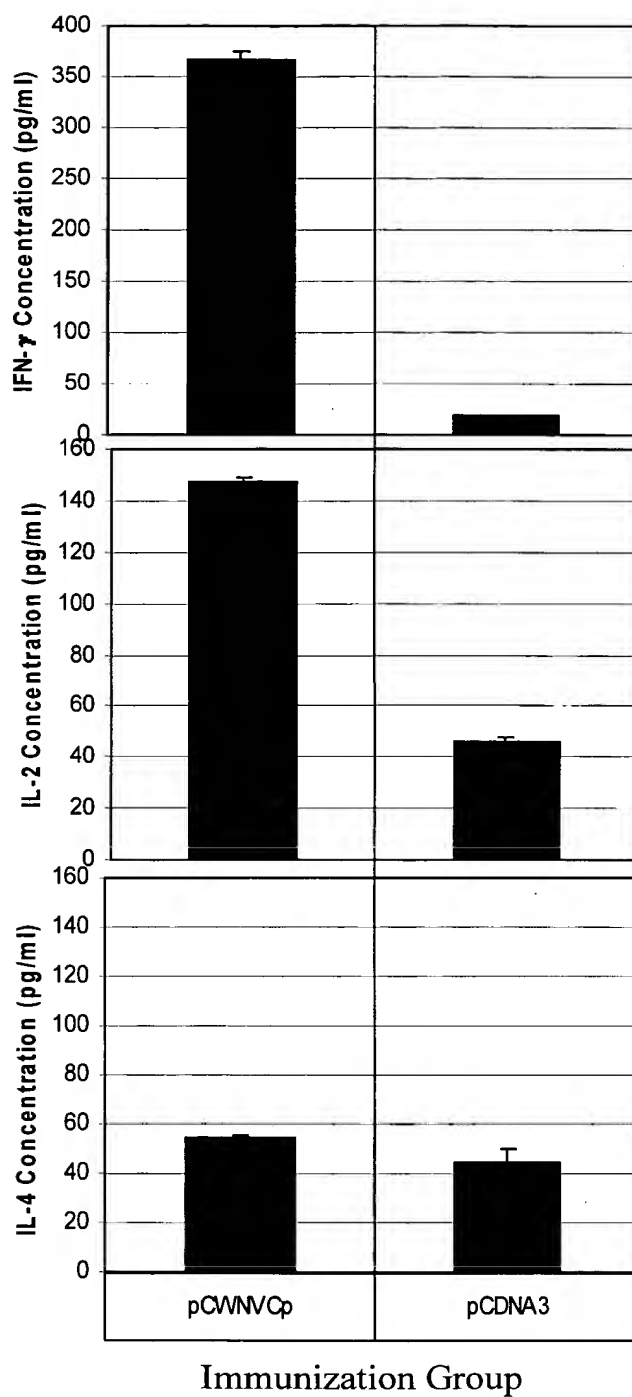


Figure 13

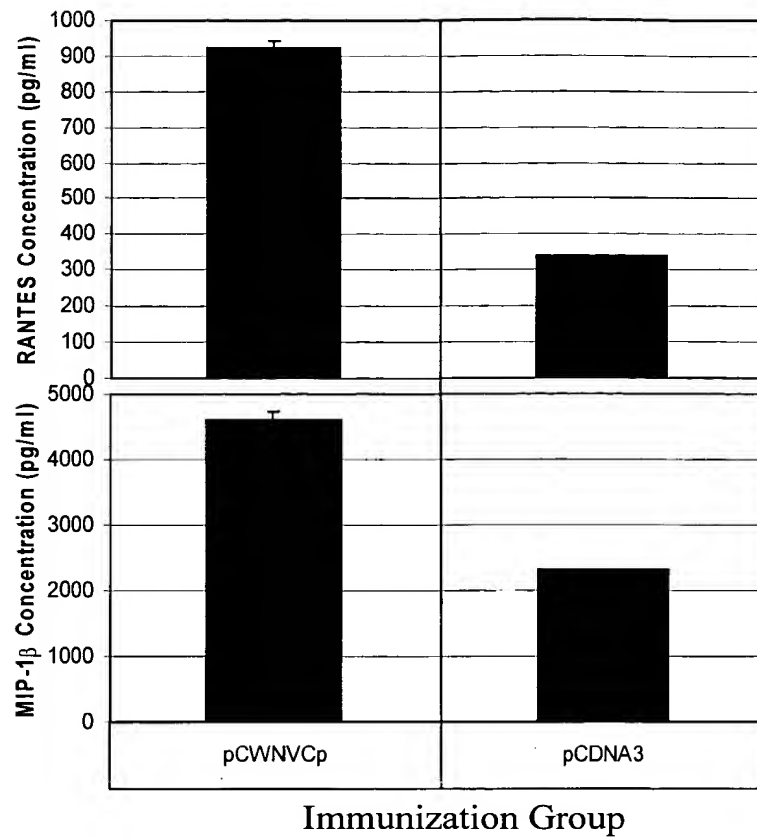


Figure 14

Fig. 15A

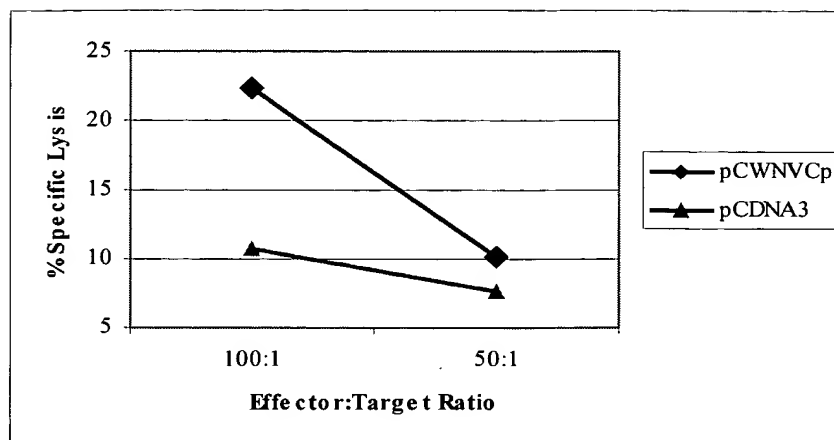


Fig. 15B

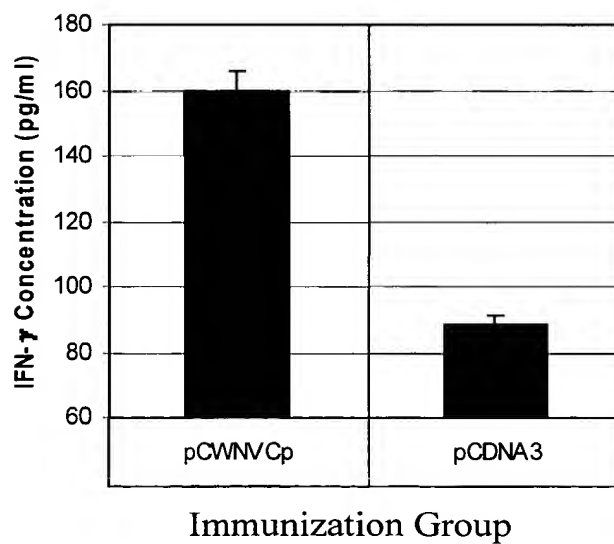


Fig. 16A

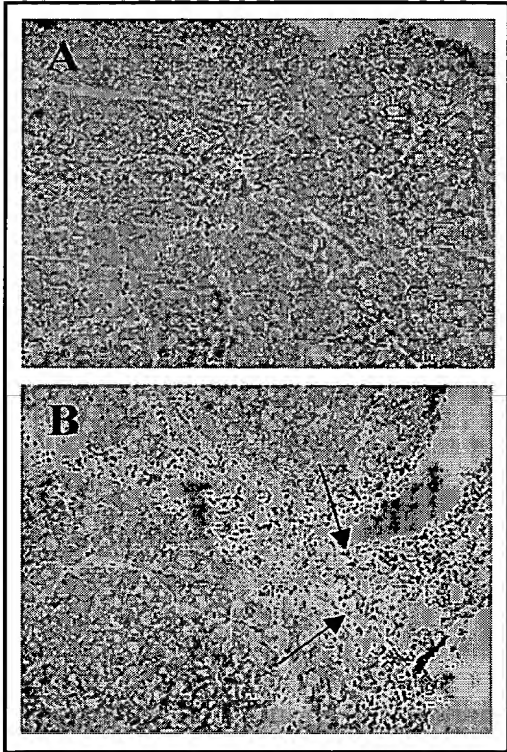


Fig. 16B

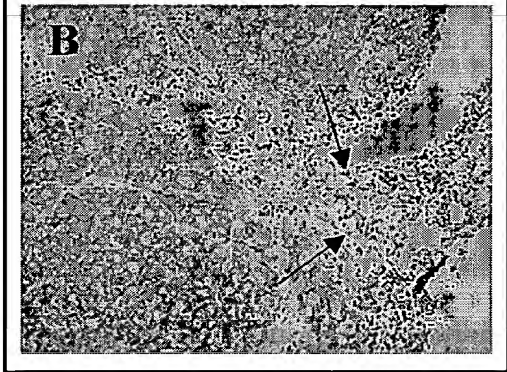


Fig. 16C

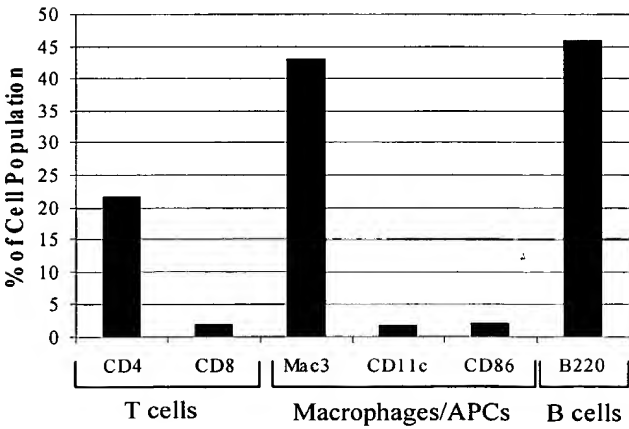
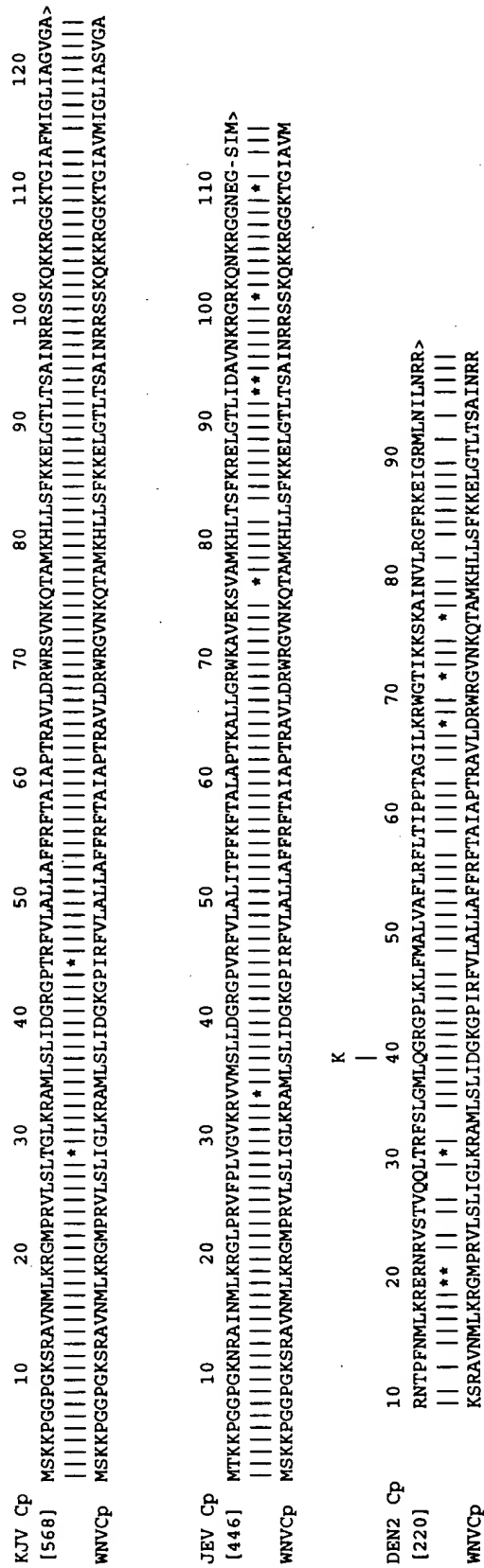


Figure 17



[illegible]

Database: UserFolder: Alignment-AC6/01

1. HIV-1 89.6 Vpr protein

[illegible]

2. Herpes Simplex virus major capsid protein

[illegible]

3. Ebola nuclear protein

3. EBOLANucl
[48]

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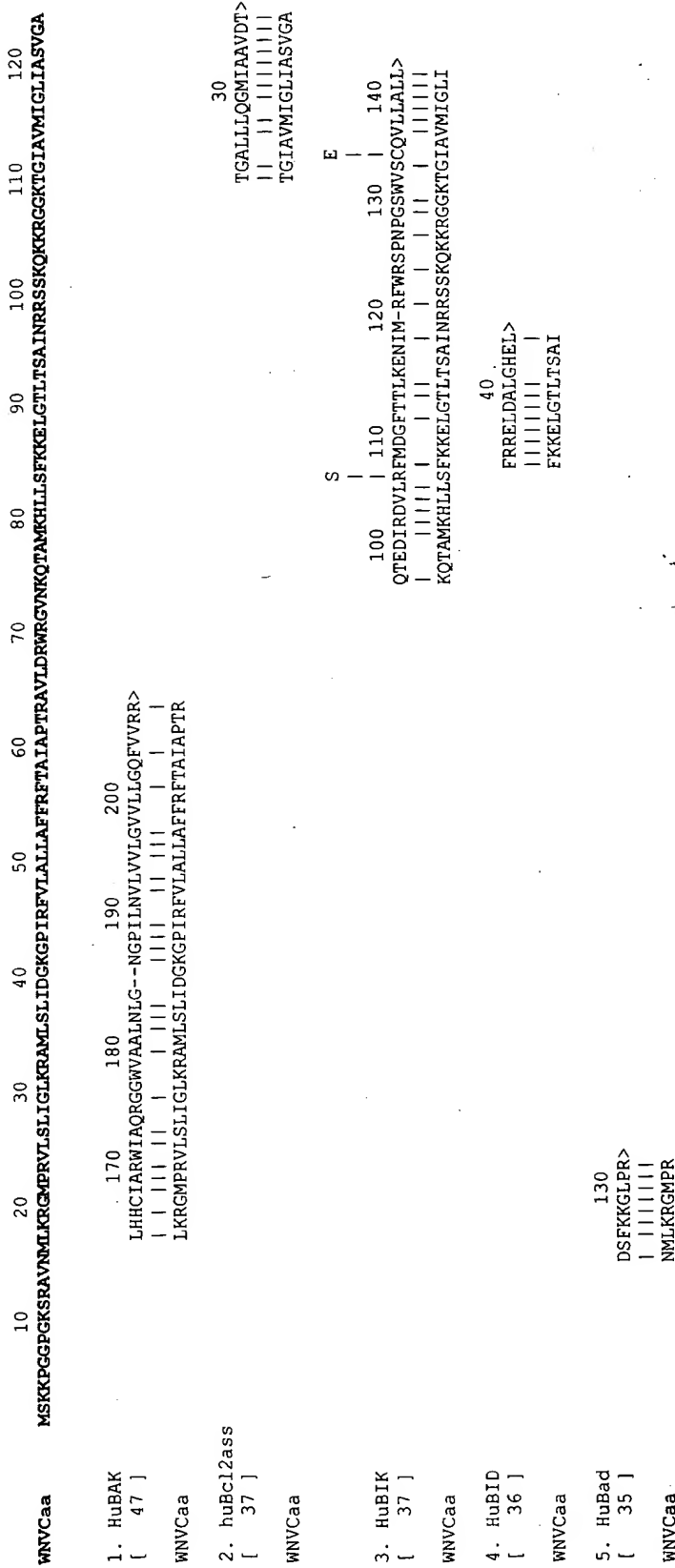
4. Ebola glycoprotein
 4. EbolaGlyc 120 130
 [30] KPDGSECLPAAPDGIRGFPR>
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5. Ebola glycoprotein
 5. EbolaGlyc
 [39]
 WNVc aa

6. Rubella capsid protein
 6. Rubellaca
 [38]
 WNVc aa

570 580 590
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 LLAFFRTAIAPTRAVLDRWGVN

270 280 290 300 310
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[illegible]

Search Analysis for Sequence: HIV-1 89.6 VpraaMatrix: pam250 matrix
 Search from 1 to 96 where origin = 1
 Date: June 15, 2001
 Time: 19:57:09
 Score Region from 1 to 96
 Maximum possible score: 515

HIV-1 89.6 MEQAPEDCGPQREPYNDWTLLEELLEELKNEAVRHPRIWLHSLGHIYETYGDTGTCVEALIRILQQLLFIHRTGCRHSRIGIIQORRTNGASKS

1. p230nonst
[{ 50 }

HIV-1 89.6

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2. WNV Caa
[45]

HIV-1 89.6

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3. Cumbermos
[36]
IIV-1 89.6

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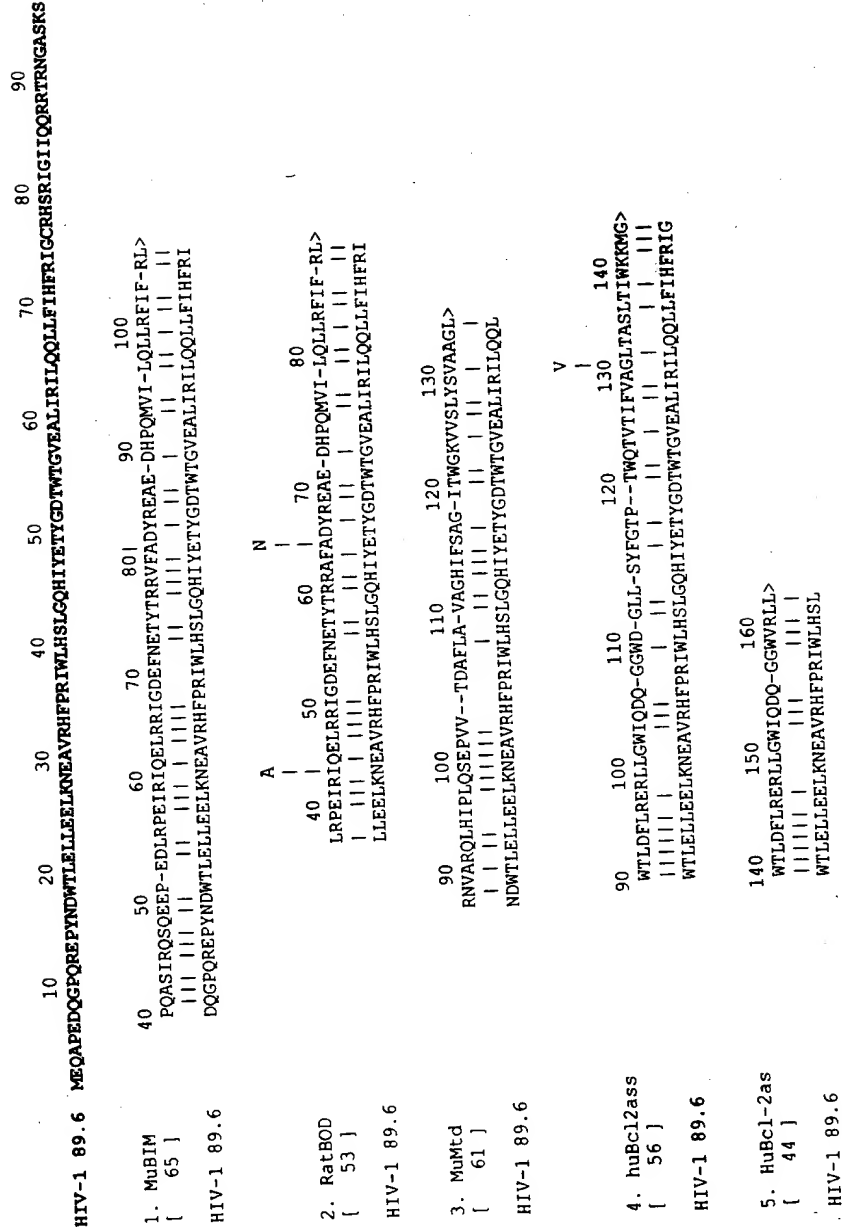
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Effect of the protein sequence to proapoptotic proteins



150 160
VFQSWDRNLGR>
| | | | |
HFPRWLHSLGQ

6. HuBad
[36]
HIV-1 89.6